

JC10 Rec'd PCT/PTO 23 DEC 2005

SEQUENCE LISTING

**SEQ ID NO: 1 - SARS Coronavirus Urbani S-protein full-length gene sequence (AY278741, 3768 bps)**

atgtttattttctattatttctactctcactagtggttagtgaccttgaccgggtgcaccactttgatgatgttcaagctcc  
taattacactcaacatacttcatctatgaggggggttactatcctgatgaatttttagatcagacactctttatttaactcag  
gattatttctccattttattctaagtgttacagggttcatactattaatcatacgtttggcaaccctgtcataccttttaaggat  
ggattattttgctgccacagagaaatcaaatgtgtccgtgggttttgggttctacatgaacaacaagtcacagtc  
ggtgattattttaacaattctactaatgtgttatcagagcatgtaactttgaattgtgtgacaaccctttcttctgtttctaa  
accatgggtacacagacacatactatgatattcgtataatgcatttaattgcactttcagtagacatactgatgccctttcgc  
ttgatgttccagaaaagtcaggtaattttaaacacttacgagagttgtgtttaaaaataaagatgggttctctatgtttataa  
gggctatcaacctatagatgtagttcgtgatctaccttctgggtttaaacctttgaaacctatttttaagttgcctcttggtatta  
acattacaatttttagagccattcttacagcctttcacctgctcaagacatttggggcacgtcagctgcagcctattttgtt  
ggctatttaagccaactacatttatgctcaagtatgatgaaaatgggtacaatcacagatgctgtgtgtgttctcaaaatcc  
actgtcgaactcaaatgctctgttaagagctttgagattgacaaaaggaattaccagaccttaatttcagggtgtgtccct  
caggagatgtgtgagattccctaattacaacattgtgtccttttggagaggttttaattgctactaaattcccttctgtcta  
tgcatggggagagaaaaaaatttcaattgtgtgtgctgattactctgtgctctacaactcaacattttttcaacctttaagt  
ctatggcgttctgccactaagtgaatgatctttgcttctccaatgtctatgcagattctttttagtcaagggagatgatgt  
aagacaaatagcgccaggacaaactggtgttatgtctgattataattataaattgccagatgattcatgggtgtgtccct  
gcttggaaactaggaacattgatgctacttcaactggaattataattataaataaggtatcttagacatggcgaagctag  
gcccttggagagacatactaatgtgcccttctccctgatggcaaaccttgacccccacctgctcttaattgttattggc  
cattaaatgattatgggttttacaccactactggcattggctaccaaccttacagagttgttagtacttctttgaacttttaaat  
gcaccggccacgggttgggtggacaaaattaccactgaccttataagaaccagtggtgcaattttaatttaaggactca  
ctggtactggtgtgttaactccttctcaagagatttcaaccttcaacaatttggccgtgatgttctgatttactgattc  
cgttcgagatcctaaaacatctgaatattagacatttcaaccttgccttttgggggtgaagtgaattacacctggaaca  
aatgcttcatctgaagtgtgttctatcaaatgttaactgcactgatgtttctacagcaattcatgcagatcaactcac  
accagcttggcgcatatatttacttgaaacaatgtattccagactcaagcaggctgtcttataggagctgagcatgtcg  
acatttctatgagtcgacatttctataggagctggcatttgtgctagtaccatacagtttcttattacgtagtactagcc  
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atttactgaatgtgctaatttgccttccaatattggtagcttttgcacacaactaaatcgtgcactctcaggattgtgtgtg  
aacaggatcgcaacacacgtgaagtgttcgtcaagtcaaacaaatgtacaaaacccaacttgaatatatttgggtgtg  
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cactgctggatggacatttgggtgtggtgctgtcttcaaataccttttctatgcaaatggcatatagggtcaatggcatt  
ggagttacccaaatgttctctatgagaacaaaaaacaatcgcaaccaatttaacaaggcgattagtaaatcaaga  
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ttaacaacttagctctaattttgtgtcaatttcaagtgtgtcaaatgatactcctttcgcgacttgataaagtcaggcgggag  
gtacaaattgacaggttaattacaggcagacttcaaagccttcaaacctatgtaacacaacaactaatcagggtgtgctga  
aatcagggtcttctgctaatttctgtgctactaaaaatgtctgagtggttcttggacaatcaaaaagagttgactttgtggaa  
agggctaccaccttatgtccttccacaagcagcccgcatggtgtgttcttctcatgtcacgtatgtgccatcccag  
gagagggaacttaccacagcgccagcaatttgcataaggcaagcatacttccctcgtgaagggtttttgtgttaaat  
ggcacttcttgggttattacacagaggaaacttcttctccacaaataattactacagacaatacatttctcaggaaattgt  
gatgtcgttattggcatcattacaacacagtttatgatcctctgcaacctgagctcgactcattcaagaagagctggac  
aagtacttcaaaaatcatacatcaccagatgttgatcttggcgacatttcaggcattaacgcttctgtcgtcaacattcaaa

aagaaattgaccgctcaatgaggtcgctaaaaatttaaatgaatcactcattgaccttcaagaattgggaaaataatgag  
caatatattaaatggccttggtatgttggtcggcttcattgctggactaattgccaicgtcatggttacaatcttgdtgtt  
gcatgactagtgttgagttgcctcaagggtgcatgctcttggtgtcttgctgcaagttgatgaggatgactctgagcc  
agttctcaagggtgtcaattacattacataa

**SEQ ID NO: 2 - Protein sequence for full length S-protein from accession number AAP13441 corresponding to the gene AY278741 (1256aa)**

MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRS  
DTLYLTQDLFLPFYSNVTGFHTINHTFGNPVIPFKDGIYFAATEKSNVVRG  
WVFGSTMNNKSQSVIIINNSTNVVIRACNFELCDNPFFAVSKPMGTQHTM  
IFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFLYVYKGYQPI  
DVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSPAQDIWGTSAAYFVG  
YLKPTTFMLKYDENGTTTDAVDCSQNPLAELKCSVKSFEDKGIYQTSNFR  
VVPBGDVVRFPNITNLCPFGEVFNATKFPSVYAWERKKISNCVADYSVLY  
NSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGDDVRQIAPGQTGVIA  
DYNKLPDDFMGCVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDI  
SNVPFSPDGKPCPPALNCYWPLNDYGFYTTTGIGYQPYRVVLSFELLNA  
PATVCGPKLSTDLIKNCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVS  
FTDSVRDPKTSEILDSPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTA  
IHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPGAGICASYH  
TVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMA  
KTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVF  
AQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTADAGF  
MKQYGECLGDINARDLCAQKFNGLTVLPPLLTDDMIAAYTAALVSGTAT  
AGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAIS  
QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRL  
DKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG  
QSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEG  
KAYFPREGVVFVNGTSWFITQRNFFSPQIITDNTFVSGNCDVVIGIINNTVY  
DPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVA  
KNLNESLIDLQELGKYEQYIKWPWYVWLGFIAGLIAIVMTILLCCMTSCC  
SCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT

**SEQ ID NO: 3 - Protein sequence for Spike protein amino acid 275-1081  
from accession number AAP13441 (807aa) (wild type, wt):**

AVDCSQNPLAELKCSVKSFEDKGIYQTSNFRVVPSGDVVRFNPITNLC  
PFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATK  
LNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLA  
WNTRNIDATSTGNYNKYR YLRHGKLRPFERDISNVPFSPDGKPCTPPALN  
CYWPLNDYGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNO  
CVNFNFNGLTGTGVLTPSSKRFQPFQFGRDVSDFTDSVRDPKTSEILDISP  
CSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGN  
NVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYT  
MSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTE  
CANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG  
GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLI  
CAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAM  
QMA YRFNGIGVTQNVLYENQKQIANQFNKAISQKESLTTTSTALGKLQDV  
VNQNAQALNTLVKQLSSNFGAIVSVLNDILSRDKVEAEVQIDRLITGRLQS  
LQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFP  
QAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVNG

**SEQ ID NO: 4 - Protein sequence for Spike protein amino acid 275-1081  
mutant with 9 potential N-linked glycosylation sites eliminated  
(807aa)(substituted Alanine shown as "a")(mutant, mt):**

AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVRFPNIaNLCP  
FGEVFaATKFPSVYAWERKKISNCVADYSVLYNsAFFSTFKCYGVSATKLN  
DLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWN  
TRNIDATSTGNYNKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCY  
WPLNDYGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCV  
NFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCS  
FGGVSVITPGTNaSEVAVLYQDVaCTDVSTAIHADQLTPAWRIYSTGNNV  
FQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTMS  
LGADSSIAYSaNTIAIPTNFaISITTEVMPVSMAKTSVDCNMYICGDSTECAN  
LLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFN  
FaQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQ  
KFNGLTVLPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQM  
AYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVN  
QNAQALNTLVKQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQ  
TYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQA  
APHGVVFLHVTYVPSQERNFaTAPAICHEGKAYFPREGVVFVFN

**SEQ ID NO: 5** - The gene sequence for Spike protein amino acid 275-1081 mutant (807aa) with native virus codons and elimination of N-glycosylation sites (2421bp) (substituted nucleotides shown capitalized):

gctgttgattgttctcaaaatccacttgctgaactcaaagctctgttaagagctttgagattgacaaaggaatttacc  
agacctctaatttcagggtgttcctcaggagatgtgtgagattccctaatattGcaaacttggtcctttggagagggtt  
tttGCCgctactaaattcccttctgtctatgcatgggagagaaaaaatttctaattgtgtgctgattactctgtgctcta  
caactcaGcattttttcaacctttaagtgtatggcgtttctgccactaagtgaatgatctttgcttccaatgtctatgca  
gattctttttagtcaaggagatgatgaagacaaatagcgccaggacaaactgggtgtattgctgattataattataaat  
tggcagatgattcatgggtgtgcttctgtgaatactaggaacattgatgctactcaactggtattataattataaat  
ataggatcttagacatggcaagcttaggccctttgagagagacatatctaatgtgcctttctcccctgatggcaaacctt  
gcacccacctgctcttaattgttattggccattaaatgattatggttttacaccactactggcattggctaccaaccttaca  
gagtgtgtagtacttctttgaacttttaaatgcaccggccacgggtgtgtgaccaaattatccactgaccttataagaac  
cagtgtgtcaattttaatttaattggactcactgggtggtgtgttaactccttctcaagagatttcaaccatttcaacaat  
ttggccgtgatgtttctgaattcactgaattccgttcgagatcctaaacatctgaaatattagacattcacctgctcttttg  
gggtgtaagtgaattacacctggaacaaatgctGcatcgaagtgtgtgtctatcaatgaatgttGCctgcactgatg  
ttttacagcaattcatgcagatcaactcacaccagcttggcgcatattctactggaacaaatgattccagactcaag  
caggctgtcttataggagctgagcatgtcgacacttctatgagtcgacattcctattggagctggcattgtgctggtta  
ccatacagttctttattacgtagtactagccaaaaatctattgtgcttatactatgtcttttaggtgctgatagtcaattgctt  
actctGCCaacaccattgctatacctactaactttGcaattagcattactacagaagtaatgcctgttttatggctaaaa  
cctccgtagattgtaatatgtacatctgcggagattctactgaatgtgctaattgcttctccaatatggtagcttttgcacac  
aactaaatcgtgcactctcaggtattgctgctgaacaggatcgcaacacacgtgaagtgttcgctcaagtcaaacaaat  
gtacaaaaccccaactttgaaatattttgggtgttttaattttGcacaatattacctgacctctaaagccaactaagagg  
tcttttataggagactgtctttaaaggtgacactcgctgatgctggcttcagaaagcaatatggcgaatgcctagggtg  
atattaatgctagagatctcattgtgcgcagaagttcaatggacttacagtgttgcacctctgctcactgatgatgatt  
gtgacctacactgtgctctagttagtggtactgccactgctggatggacatttgggtgctggcgctgctcttcaaatacctt  
ttgctatgcaaatggcatatagggtcaatggcattggagttacccaaaatgttctctatgagaacaaaaacaaatcgcca  
accaatttaacaaggcgattagtcaaatcaagaatcacttacaacaacatcaactgcattgggcaagctgaagacgtt  
gttaaccagaatgtcaagcattaaacacactgtttaaacaacttagctctaattttgggtgcaatttcaagtgtgctaaatga  
tatcctttcgcgacttgataaagtcgaggcggaggtacaaattgacagggttaattacaggcagacttcaaaagccttcaaa  
cctatgtaacacaacaactaatcagggtgctgaaatcagggtcttctgctaatcttgcgtactaaaaatgtctgagtgtgt  
tcttgacaatcaaaaagagttgacttttgggaaagggtaccaccttatgtccttccacaagcagccccgatgggtg  
ttgtctctacatgtcacgtatgtgccatccaggagagggaacttcGccacagcgccagcaatttgcattgaaggcaa  
agcatacttccctgtgaagggtgttttgtgttaattggc

**SEQ ID NO: 6 - The gene sequence for Spike protein amino acid 275-1081 mutant (807aa) with altered codon usage to enhance expression and elimination of N-glycosylation sites (2421bp):**

GCCGTGGACTGCTCCCAGAACCCCTGGCCGAGCTGAAGTGCTCCGTGAAGT  
CCTTCGAGATCGACAAGGGCATCTACCAGACCTCCAACCTCCGCGTGGTGCCCTC  
CGGCGACGTGGTGCGCTTCCCCAACATCGCCAACCTGTGCCCTTCGGCGAGGTG  
TTCGCCGCCACCAAGTTCCCCTCCGTGTACGCCTGGGAGCGCAAGAAGATCTCCA  
ACTGCGTGGCCGACTACTCCGTGCTGTACAACCTCCGCCTTCTTCTCCACCTTCAA  
GTGCTACGGCGTGTCCGCCACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTAC  
GCCGACTCCTTCGTGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCCGGCCAGA  
CCGGCTGATCGCCGACTACAACCTACAAGCTGCCCGACGACTTCATGGGCTGCGT  
GCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGCAACTACAACCTAC  
AAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCCTTCGAGCGCGACATCTCCA  
ACGTGCCCTTCTCCCCGACGGCAAGCCCTGCACCCCCCGCCCTGAAGTGTCTA  
CTGGCCCCTGAACGACTACGGCTTCTACACCACCACCGGCATCGGCTACCAGCCC  
TACCGCGTGGTGGTGTCTCCTTCGAGCTGCTGAACGCCCCCGCCACCGTGTGCG  
GCCCCAAGCTGTCCACCGACCTGATCAAGAACCAGTGCCTGAACCTTCAACTTCAA  
CGCCCTGACCGGCACCGCGTGTGACCCCCCTCCTCAAGCGCTTCCAGCCCTTC  
CAGCAGTTCGGCCGCGACGTGTCCGACTTCACCGACTCCGTGCGCGACCCCAAGA  
CCTCCGAGATCCTGGACATCTCCCCCTGCTCCTTCGGCGGCGTGTCCGTGATCAC  
CCCCGGCACCAACGCCGCCCTCCGAGGTGGCCGTGCTGTACCAGGACGTGGCCTGC  
ACCGACGTGTCCACCGCCATCCACGCCGACGAGCTGACCCCCGCCTGGCGCATCT  
ACTCCACCGGCAACAACGTGTTCCAGACCCAGGCCGGCTGCCTGATCGGCGCCGA  
GCACGTGGACACCTCCTACGAGTGCAGATCCCCATCGGCGCCGGCATCTGCGCC  
TCCTACCACACCGTGTCCCTGCTGCGCTCCACCTCCCAGAACTCCATCGTGGCCT  
ACACCATGTCCCTGGGCGCCGACTCCTCCATCGCCTACTCCGCCAACACCATCGC  
CATCCCCACCAACTTCGCCATCTCCATCACCACCGAGGTGATGCCCGTGTCCATG  
GCCAAGACCTCCGTGGACTGCAACATGTACATCTGCGGCGACTCCACCGAGTGC  
CCAACCTGCTGCTGCAGTACGGCTCCTTCTGCACCCAGCTGAACCGCGCCCTGTC  
CGGCATCGCCGCGGAGCAGGACCGCAACACCCGCGAGGTGTTGCGCCAGGTGAAG  
CAGATGTACAAGACCCCCACCCCTGAAGTACTTCGGCGGCTTCAACTTCGCCCAGA  
TCCTGCCCAGCCCCCTGAAGCCACCAAGCGCTCCTTCATCGAGGACCTGCTGTT  
CAACAAGGTGACCCTGGCCGACGCCGGCTTCATGAAGCAGTACGGCGAGTGCCTG  
GGCGACATCAACGCCCCGCGACCTGATCTGCGCCCAGAAGTTCAACGGCCTGACCG  
TGCTGCCCCCCTGCTGACCGACGACATGATCGCCGCCTACACCGCCGCCCTGGT  
GTCCGGCACCGCCACCGCCGGCTGGACCTTCGGCGCCGGCGCCGCCCTGCAGATC  
CCCTTCGCCATGCAGATGGCCTACCGCTTCAACGGCATCGGCGTGACCCAGAACG  
TGCTGTACGAGAACCAGAAGCAGATCGCCAACCAAGTTCAACAAGGCCATCTCCCA  
GATCCAGGAGTCCCTGACCACCACCTCCACCGCCCTGGGCAAGCTGCAGGACGTG  
GTGAACCAGAACGCCCAGGCCCTGAACACCCTGGTGAAGCAGCTGTCTCCAAC  
TCGGCGCCATCTCCTCCGTGCTGAACGACATCCTGTCCCGCCTGGACAAGGTGGA  
GGCCGAGGTGCAGATCGACCGCCTGATCACCGGCCGCCTGCAGTCCCTGCAGACC  
TACGTGACCCAGCAGCTGATCCGCGCCGCGAGATCCGCGCCTCCGCCAACCTGG  
CCGCCACCAAGATGTCCGAGTGCCTGCTGGGCCAGTCCAAGCGCGTGGACTTCTG  
CGGCAAGGGCTACCACCTGATGTCTTCCCCAGGCCGCCCCCACGGCGTGGTG  
TTCCTGCACGTGACCTACGTGCCCTCCCAGGAGCGCAACTTCGCCACCGCCCCCG  
CCATCTGCCACGAGGGCAAGGCCTACTTCCCCCGGAGGGCGTGTTCGTGTTCAA  
CGGC

**SEQ ID NO: 7** - Potential N-glycosylation sites within the protein sequence of the Spike protein amino acid 275-1081 (807aa) (wild type, wt) with potential N-glycosylation sites underlined.

AVDCSQNPLAELKCSVKSF<sup>1</sup>EIDKGIYQTSNFRVVP<sup>2</sup>SGDVVRFP<sup>3</sup>NITNLC  
 PFGEVFNAT<sup>4</sup>KFPSVYAWERKKISNCVADYSVL<sup>5</sup>YN<sup>6</sup>STFFSTFKCYGVSATK  
 LNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKL<sup>7</sup>PDDFMGCVLA  
 WNTRNIDATSTGN<sup>8</sup>YNYKYRYLRHGKLRP<sup>9</sup>FERDISNVPFSPDGK<sup>10</sup>PCTPPALN  
 CYWPLNDYGFYTTT<sup>11</sup>GIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQ  
 CVN<sup>12</sup>FNFNGLTGTGVLTPSSKRFQPFQ<sup>13</sup>QFGRDVSDF<sup>14</sup>TDSVRDPKTSEILD<sup>15</sup>ISP  
 CSF<sup>16</sup>GGVSVITPGT<sup>17</sup>NA<sup>18</sup>SEVAVLYQDV<sup>19</sup>NCTDVSTAIHADQLTPAWRIYSTGN  
 NVFQTQAGCLIGAEHVDTSYEC<sup>20</sup>DIPIGAGICASYHTVSL<sup>21</sup>LRSTSQKSIVAYT  
 MSLGADSSIAYSN<sup>22</sup>NTIAIPTN<sup>23</sup>FSISITTEVMPVSM<sup>24</sup>AKTSVDCNMYICGDSTE  
 CANLL<sup>25</sup>LQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG  
 GF<sup>26</sup>NFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLI  
 CAQKF<sup>27</sup>NGLTVLPPLLTD<sup>28</sup>MIAAYTAALVSGTATAGWTFGAGAALQIPFAM  
 QMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDV  
 VNQNAQALNTLVKQLSSNFGA<sup>29</sup>ISSVLNDILSR<sup>30</sup>LDKVEAEVQIDRLITGRLQS  
 LQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLSFP  
 QAAPHGVVFLHVTYVPSQERN<sup>31</sup>FTTAPAICHEGKAYFPREGVVFVNG

**SEQ ID NO: 8 Amino acid sequence of Region II peptide**

VLYN<sup>32</sup>SAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADY  
 NYKL<sup>33</sup>PDDFMGCVLAWNTRNIDATSTGN<sup>34</sup>YNYKYRYLRHGKLRP<sup>35</sup>FERDISNVPFSP  
 DGK<sup>36</sup>PCTPPALNCYWPLNDYGFYTTT<sup>37</sup>GIGYQPYRVVLSFELLNAPATVCGPKLST  
 DLIKNQCVN<sup>38</sup>FNFNGLTGTGVLTPSSKRFQPFQ<sup>39</sup>QFGRDVSDF<sup>40</sup>TDSVRDPKTSEILD<sup>41</sup>IS  
 PCSF<sup>42</sup>GGVSVITPGTNAASEVAVLYQDV

**SEQ ID NO: 9 Amino acid sequence of Region III peptide**

AEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRSFIEDLLFNKV  
 TLADAGFMKQYGECLGDINARDLICAQKF<sup>43</sup>NGLTVLPPLLTD<sup>44</sup>MIAAYTAALVSGT  
 ATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQ  
 ESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGA<sup>45</sup>ISSVLNDILSR<sup>46</sup>LDKVEAEV  
 QIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKG  
 YHL

**SEQ ID NO: 10 Amino acid sequence of Region IV peptide**

VLYN<sup>47</sup>SAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADY  
 NYKL<sup>48</sup>PDDFMGCVLAWNTRNIDATSTGN<sup>49</sup>YNYKYRYLRHGKLRP<sup>50</sup>FERDISNVPFSP  
 DGK<sup>51</sup>PCTPPALNCYWPLNDYGFYTTT<sup>52</sup>GIGYQPYRVVLSFELLNAPATVCGPKLST  
 DLIKNQCVN<sup>53</sup>FNFNGLTGTGVLTPSSKRFQPFQ<sup>54</sup>QFGRDVSDF<sup>55</sup>TDSVRDPKTSEILD<sup>56</sup>IS  
 PCSF<sup>57</sup>GGVSVITPGTNAASEVAVLYQDVACTDVSTAIHADQLTPAWRIYSTGNNVF



QTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSS  
IAYSANTIAIPTNFAISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCT  
QLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQLPDPLKPTKRS  
FIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIA  
AYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIA  
NQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDI  
LSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQ  
SKRVDFCGKGYHL

**SEQ ID NO: 11 Amino acid sequence of Region II peptide from Spike protein from accession number AAP13441(wild type)**

VLNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQ  
TGVADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHGKLRP  
FERDISNVPFSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVLSF  
ELLNAPATVCGPKLSTD LIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFG  
RDVSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDV

**SEQ ID NO: 12 Amino acid sequence of Region III peptide from Spike protein from accession number AAP13441(wild type)**

AEQDRNTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIED  
LLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMI  
AAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYEN  
QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNF  
GAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASAN  
LAATKMSECVLGQSKRVDFCGKGYHL

**SEQ ID NO: 13 Amino acid sequence of Region IV peptide from Spike protein from accession number AAP13441(wild type):**

VLNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTG  
VIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHGKLRPFE  
RDISNVPFSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVLSFEL  
LNAPATVCGPKLSTD LIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRD  
VSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDV  
STAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICA  
SYHTVSLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVS  
MAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTRE  
VFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADA  
GFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGT  
ATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKA  
ISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILS  
RLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECV  
LGQSKRVDFCGKGYHL

**SEQ ID NO: 14 Amino acid sequence of Region IV peptide from Spike protein from accession number AAP13441(wild type):**

AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVRFPNITNLCPCFG  
EVFNATKFPSPVYAWERKKISNCVADYSVLNSTFFSTFKCYGVSATKLND  
LCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNT  
RNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCPTPALNCY  
WPLNDYGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCV  
NFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFDTSVRDPKTSEILDISPCS  
FGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNN  
VFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTM  
SLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECA  
NLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGF  
NFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICA  
QKFNGLTVLPLLTDDMLAAAYTAALVSGTATAGWTFGAGAALQIPFAMQ  
MAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVV  
NQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSL  
QTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHL

**SEQ ID NO: 15 Linker for nucleotide primer oligo #1**

TCGCTCGAGAAAAGAGTGCTCTACAACCTCAGCATTT

**SEQ ID NO: 16 Linker for nucleotide primer oligo #2**

ATCTCTAGATTAAACATCTTGATATAGAACAGC

**SEQ ID NO: 17 Linker for nucleotide primer oligo #3** TCGCTCGAG

AAAAGAGCTGAACAGGATCGCAACACA

**SEQ ID NO: 18 Linker for nucleotide primer oligo #4**

ATCTCTAGATTAAAGGTGGTAGCCCTTTCC

**SEQ ID NO: 19 SARS Spike Glycoprotein Fragment synthetic DNA sequence with N-lined glycosylation site mutations (2421 bp)**

GCCGTGGACTGCTCCCAGAACCCACTGGCCGAGCTGAAGTGCTCCGTGA  
AGTCCTTCGAGATCGACAAGGGCATCTACCAGACCTCCAACCTCCGCGTG  
GTGCCATCCGGCGACGTGGTGCGCTTCCCAAACATCGCCAACCTGTGCC

CATTCGGCGAGGTGTTTCGCCGCCACCAAGTTCCCATCCGTGTACGCCTG  
GGAGCGCAAGAAGATCTCCAACCTGCGTGGCCGACTACTCCGTG  
CTGTACAACTCCGCCTTCTTCTCCACCTTCAAGTGCTACGGCGTGTCCGC  
CACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTACGCCGACTCCTTCG  
TGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCAGGCCAGACCGGCGT  
GATCGCCGACTACAACTACAAGCTGCCAGACGACTTCATGGGCTGCGTG  
CTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACTACA  
ACTACAAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCATTCGAGCG  
CGACATCTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACCCAC  
CAGCCCTGAACTGCTACTGGCCACTGAACGACTACGGCTTCTACACCACC  
ACCGGCATCGGCTACCAGCCATACCGCGTGGTGGTGTCTCTTCGAGC  
TGCTGAACGCCCCAGCCACCGTGTGCGGCCCAAAGCTGTCCACCGACCT  
GATCAAGAACCAGTGCGTGAACCTTCAACTTCAACGGCCTGACCGGCACC  
GGCGTGCTGACCCCATCCTCCAAGCGCTTCCAGCCATTCCAGCAGTTCGG  
CCGCGACGTGTCCGACTTCACCGACTCCGTGCGCGACCCAAAGACCT  
CCGAGATCCTGGACATCTCCCCATGCTCCTTCGGCGGCGTGTCCGTGATC  
ACCCAGGCACCAACGCCGCCTCCGAGGTGGCCGTGCTGTACCAGGACG  
TGGCCTGCACCGACGTGTCCACCGCCATCCACGCCGACCAGCTGACCCC  
AGCCTGGCGCATCTACTCCACCGGCAACAACGTGTTCCAGACCCAGGCC  
GGCTGCCTGATCGGCGCCGAGCACGTGGACACCTCCTACGAGT  
GCGACATCCCAATCGGCGCCGGCATCTGCGCCTCCTACCACACCGTGTC  
CCTGCTGCGCTCCACCTCCCAGAAGTCCATCGTGGCCTACACCATGTCCC  
TGGGCGCCGACTCCTCCATCGCCTACTCCGCCAACACCATCGCCATCCCA  
ACCAACTTCGCCATCTCCATCACCACCGAGGTGATGCCAGTGTCCATGGC  
CAAGACCTCCGTGGACTGCAACATGTACATCTGCGGCGACTCCACCGAG  
TGCGCCAACCTGCTGCTGCAGTACGGCTCCTTCTGCACCCAGCTGAACCG  
CGCCCTGTCCGGCATCGCCGCCGAGCAGGACCGCAACACCCGCGAGGTG  
TTCGCCCAGGTGAAGCAGATGTACAAGACCCCAACCCTGAAGTACTTCG  
GCGGCTTCAACTTCGCCCAGATCCTGCCAGACCCACTGAAGCCAACCAA  
GCGCTCCTTCATCGAGGACCTGCTGTTCAACAAGGTGACCCTGGCCGAC  
GCCGGCTTCATGAAGCAGTACGGCGAGTGCCTGGGCGACATCAACGCCC  
GCGACCTGATCTGCGCCCAGAAGTTCAACGGCCTGACCGTGCTGCCACC  
ACTGCTGACCGACGACATGATCGCCGCCTACACCGCCGCCCTGGTGTC  
CGGCACCGCCACCGCCGGCTGGACCTTCGGCGCCGGCGCCGCCCTGCAG  
ATCCCATTCGCCATGCAGATGGCCTACCGCTTCAACGGCATCGGCGTGAC  
CCAGAACGTGCTGTACGAGAACCAGAAGCAGATCGCCAACCAGTTCAAC  
AAGGCCATCTCCAGATCCAGGAGTCCCTGACCACCACCTCCACCGCCCT  
GGGCAAGCTGCAGGACGTGGTGAACCAGAACGCCAGGCCCT  
GAACACCCTGGTGAAGCAGCTGTCTTCCAACCTTCGGCGCCATCTCTCCG  
TGCTGAACGACATCCTGTCCCGCCTGGACAAGGTGGAGGCCGAGGTGCA  
GATCGACCGCCTGATCACC GGCCGCCTGCAGTCCCTGCAGACCTACGTG  
ACCCAGCAGCTGATCCGCGCCGCCGAGATCCGCGCCTCCGCCAACCTGG  
CCGCCACCAAGATGTCCGAGTGCGTGCTGGGCCAGTCCAAGCG  
CGTGGACTTCTGCGGCAAGGGCTACCACCTGATGTCTTCCCACAGGCC  
GCCCCACACGGCGTGGTGTTCTTCTGCACGTGACCTACGTGCCATCCCAGG  
AGCGCAACTTCGCCACCGCCCCAGCCATCTGCCACGAGGGCAAGGCCTA  
CTTCCCACGCGAGGGCGTGTTCTGTGTTCAACGGC

**SEQ ID NO: 20**

SARs Spike glycoprotein Fragment I protein sequence without the N-linked glycosylation sites (807 amino acids encoded by SEQ ID NO: 19):

AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVPSGDVVRFPNIANLCPFGEVFAATKFPSVYA  
WERKKISNCVADYSVLVNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGV  
IADYNYKLPDDFMGCVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDISNVPFSPDGKPCPT  
PALNCYWPLNDYGFTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNCVNFNFNGLTG  
TGVLTSSKRFQPFQFGRDVSDFDTSVRDPKTSEILDSPCSFGGVSIVITPGTNAASEVAVLYQ  
DVACTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECPIGAGICASYHTVSL  
RSTSQKSIVAYTMSLGADSSIAYSANTIAIPTNFAISITTEVMPVSMAKTSVDCNMYICGDESTECANL  
LLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRSFI  
EDLLFNKVTADAGFMKQYGECLGDINARDLCAQKFNGLTVLPPLLTDMDIAAYTAALVSGTATA  
GWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQ  
DVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA  
EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQAAPHGVVFLHVTYVPSQERNFATAPAI  
CHEGKAYFPREGVVFVNG

**SEQ ID NO: 21: SARs Spike glycoprotein Fragment II synthetic DNA sequence with N-linked glycosylation site mutations (744bps):**

GTGCTGTACAACTCCGCCTTCTTCTCCACCTTCAAGTGCTACGGCGTGTC  
CGCCACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTACGCCGACTCCT  
TCGTGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCAGGCCAGACCGG  
CGTGATCGCCGACTACAACTACAAGCTGCCAGACGACTTCATGGGCTGC  
GTGCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACT  
ACAACTACAAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCATTCGA  
GCGCGACATCTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACC  
CCACCAGCCCTGAACTGCTACTGGCCACTGAACGACTACGGCTTCTACAC  
CACCACCGGCATCGGCTACCAGCCATACCGCGTGGTGGTGTCTCCTTC  
GAGCTGCTGAACGCCCCAGCCACCGTGTGCGGCCCAAAGCTGTCCACCG  
ACCTGATCAAGAACCAGTGCCTGAACCTTCAACTTCAACGGCCTGACCGGC  
ACCGGCGTGCTGACCCCATCCTCCAAGCGCTTCCAGCCATTCCAGCAGTT  
CGGCCGCGACGTGTCCGACTTCACCGACTCCGTGCGCGACCCAAAGACC  
TCCGAGATCCTGGACATCTCCCATGCTCCTTCGGCGGCGTGCTCCGTGAT  
CACCCAGGCACCAACGCCGCCTCCGAGGTGGCCGTGCTGTACCAGGAC  
GTG

**SEQ ID NO: 22: SARs Spike glycoprotein Fragment II protein sequence without the N-linked glycosylation sites (248 amino acids, encoded by SEQ ID 21):**

VLVNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVADYNYKLPDDFMG  
CVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDISNVPFSPDGKPCPTPALNCYWPLNDYG  
FYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNCVNFNFNGLTGTVLTSSKRFQPF  
QQFGRDVSDFDTSVRDPKTSEILDSPCSFGGVSIVITPGTNAASEVAVLYQDV

**SEQ ID NO: 23: SARS Spike glycoprotein Fragment III synthetic DNA sequence with N-linked glycosylation site mutations (834 bps):**

GCCGAGCAGGACCGCAACACCCGCGAGGTGTTGCCCCAGGTGAAGCAGA  
TGTAACAAGACCCCAACCCTGAAGTACTTCGGCGGCTTCAACTTCGCCCAG  
ATCCTGCCAGACCCACTGAAGCCAACCAAGCGCTCCTTCATCGAGGACCT  
GCTGTTCAACAAGGTGACCCTGGCCGACGCCGGCTTCATGAAGCAGTAC  
GGCGAGTGCTGGGCGACATCAACGCCCGCGACCTGATCTGCGCCCAGA  
AGTTCAACGGCCTGACCGTGCTGCCACCACTGCTGACCGACGACATGAT

CGCCGCCTACACCGCCGCCCTGGTGTCCGGCACCGCCACCGCCGGCTGG  
ACCTTCGGCGCCGGCGCCGCCCTGCAGATCCCATTTCGCCATGCAGATGG  
CCTACCGCTTCAACGGCATCGGCGTGACCCAGAACGTGCTGTACGAGAA  
CCAGAAGCAGATCGCCAACCAGTTCAACAAGGCCATCTCCCAGATCCAG  
GAGTCCCTGACCACCACCTCCACCGCCCTGGGCAAGCTGCAGGACGTGG  
TGAACCAGAACGCCAGGCCCTGAACACCCTGGTGAAGCAGCTGTCCTC  
CAACTTCGGCGCCATCTCCTCCGTGCTGAACGACATCCTGTCCCGCCTGG  
ACAAGGTGGAGGCCGAGGTGCAGATCGACCGCCTGATCACCGGCCGCCCT  
GCAGTCCCTGCAGACCTACGTGACCCAGCAGCTGATCCGCGCCGCCGAG  
ATCCGCGCCTCCGCCAACCTGGCCGCCACCAAGATGTCCGAGTGCGTGC  
TGGGCCAGTCCAAGCGCGTGGACTTCTGCGGCAAGGGCTACCACCTG

**SEQ ID NO: 24: SARs Spike glycoprotein Fragment III protein sequence without the N-linked glycosylation sites (278 amino acids, encoded by SEQ ID NO: 23):**

AEQDRNTREVFQVQKMYKTPTLKYFGGFNFAQILPDPLKPTKRSFIEDLLFNKVTLDAGFMKQ  
YGECLGDINARDLICAQKFNGLTVPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQ  
MAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTSTALGKLQDVVNQNAQALNTLVKQLS  
SNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG  
QSKRVDFCGKGYHL

**SEQ ID NO: 25: SARs Spike glycoprotein Fragment IV synthetic DNA sequence with N-linked glycosylation site mutations (2034 bps):**

GTGCTGTACAACCTCCGCTTCTTCCACCTTCAAGTGCTACGGCGTGTCCGCCACCAAGCT  
GAACGACCTGTGCTTCTCAACGTGTACGCCGACTCCTTCGTGGTGAAGGGCGACGACGTG  
CGCCAGATCGCCCCAGGCCAGACCGGCGTGATCGCCGACTACAACTACAAGCTGCCAGAC  
GACTTCATGGGCTGCGTGCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCA  
ACTACAACCTACAAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCATTCGAGCGCGACAT  
CTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACCCACCAGCCCTGAACTGCTAC  
TGGCCACTGAACGACTACGGCTTCTACACCACCAACCGGCATCGGCTACCAGCCATACCGCG  
TGGTGGTGCTGTCTTCGAGCTGCTGAACGCCCGCCAGCCACCGTGTGCGGCCCAAGCTGTC  
CACCGACCTGATCAAGAACCAGTGCGTGAACCTTCAACTTCAACGGCCTGACCGGCACCGGC  
GTGCTGACCCCATCTCCAAGCGCTTCCAGCCATTCCAGCAGTTCCGGCCGCGACGTGTCCG  
ACTTCACCGACTCCGTGCGCGACCCAAAGACCTCCGAGATCCTGGACATCTCCCCATGCTC  
CTTCGGCGGCGTGCTCGTGATCACCCAGGCACCAACGCCGCTCCGAGGTGGCCGTGCT  
GTACCAAGGACGTGGCCTGCACCGACGTGTCCACCGCCATCCACGCCGACGAGCTGACCCC  
AGCCTGGCGCATCTACTCCACCGGCAACAACGTGTTCCAGACCCAGGCCGGCTGCCTGATC  
GGCGCCGAGCAGTGACACCTCTACGAGTGCGACATCCCAATCGGCGCCGCGCATCTGC  
GCCTCTACCACACCGTGCTCCTGCTGCGCTCCACCTCCAGAAAGTCCATCGTGCC TACA  
CCATGTCCCTGGGCGCGGACTCCTCCATCGCCTACTCCGCCAACACCATCGCCATCCCAAC  
CAACTTCGCCATCTCCATCACCAACCGAGGTGATGCCAGTGTCATGGCCAAGACCTCCGTG  
GACTGCAACATGTACATCTGCGGCGACTCCACCGAGTGCGCCAACCTGCTGCTGCAGTACG  
GCTCCTTCTGCACCCAGCTGAACCGCGCCCTGTCCGGCATCGCCGCCGAGCAGGACCGCA  
ACACCCGCGAGGTGTTCCGCCAGGTGAAGCAGATGTACAAGACCCCAACCCTGAAGTACTT  
CGGCGGCTTCAACTTCGCCAGATCCTGCCAGACCCACTGAAGCCAACCAAGCGCTCCTTC  
ATCGAGGACCTGCTGTTCAACAAGGTGACCCTGGCCGACGCCGGCTTCATGAAGCAGTACG  
GCGAGTGCTGGGCGACATCAACGCCCGCGACCTGATCTGCGCCAGAAAGTTCAACGGCC  
TGACCGTGCTGCCACCACTGCTGACCGACGACATGATCGCCGCCTACACCGCCGCCCTGGT  
GTCCGGCACCGCCACCGCCGGCTGGACCTTCGGCGCCGGCGCCGCCCTGCAGATCCCAT  
CGCCATGCAGATGGCCTACCGCTTCAACGGCATCGGCGTGACCCAGAACGTGCTGTACGAG  
AACCAGAAGCAGATCGCCAACCAGTTCAACAAGGCCATCTCCAGATCCAGGAGTCCCTGA  
CCACCACCTCCACCGCCCTGGGCAAGCTGCAGGACGTGGTGAACCAGAACGCCAGGCC  
TGAACACCCTGGTGAAGCAGCTGTCTCCAACCTTCGGCGCCATCTCCTCCGTGCTGAACGA  
CATCCTGTCCCGCCTGGACAAGGTGGAGGCCGAGGTGCAGATCGACCGCCTGATCACCGG  
CCGCTGCAGTCCCTGCAGACCTACGTGACCCAGCAGCTGATCCGCGCCGCCGAGATCCG  
CGCCTCCGCCAACCTGGCCGCCACCAAGATGTCGAGTGCGTGCTGGGCCAGTCCAAGCG  
CGTGACTTCTGCGGCAAGGGCTACCACCTG

SEQ ID NO: 26: SARs Spike glycoprotein Fragment IV protein sequence without the N-linked glycosylation sites (678 amino acids, encoded by SEQ ID NO: 25):  
VLYNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMG  
CVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDISNVPFSPDGKPTPPALNCYWPLNDYG  
FYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNCVNFNFNGLTGTGVLTPSSKRFQPF  
QQFGRDVSDFDTSVRDPKTSEILDSPCSFGGVSVITPGTNAASEVAVLYQDVACTDVSTAIHADQ  
LTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSL  
GADSSIAYSANTIAIPTNFAISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRA  
LSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRSFIEDLLFNKVTADAG  
FMKQYGECLGDINARDLCAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPF  
AMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLV  
KQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSE  
CVLGQSKRVDFCGKGYHL